

1/28
SEQUENCE LISTING

<110> Meiji Seika Kaisha, Ltd.

<120> Transformants that produce secondary metabolites
modified by a functional group(s) and novel
biosynthesis genes

<130> 127185PX

<140>

<141>

<150> 276314/1999

<151> 1999-09-29

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 2061

<212> DNA

<213> Streptomyces venezuelae

<220>

<221> CDS

<222> (1).. (2058)

<400> 1

atg cgc acg ctt ctg atc gac aac tac gac tcg ttc acc cac aac ctg 48

Met Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Phe Thr His Asn Leu

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5

10

15

ttc cag tac atc ggc gag gcc acc ggg caa ccc ccc gtc gtc gtg ccc 96

Phe Gln Tyr Ile Gly Glu Ala Thr Gly Gln Pro Pro Val Val Val Pro

20

25

30

aac gac gcc gac tgg tcg cgg ctg ccc gtc gag gac ttc gac gcg atc 144

Asn Asp Ala Asp Trp Ser Arg Leu Pro Val Glu Asp Phe Asp Ala Ile

35

40

45

gtc gtg tcc ccg ggc ccc ggc agc ccc gac cgg gaa cgg gac ttc gga 192

Val Val Ser Pro Gly Pro Gly Ser Pro Asp Arg Glu Arg Asp Phe Gly

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55

60

atc agc cgc cgg gcg atc acc gac agc ggc ctg ccc gtc ctc ggc gtc 240

Ile Ser Arg Arg Ala Ile Thr Asp Ser Gly Leu Pro Val Leu Gly Val

65

70

75

80

tgc ctc ggc cac cag ggc atc gcc cag ctc ttc ggc gga acc gtc ggc 288

Cys Leu Gly His Gln Gly Ile Ala Gln Leu Phe Gly Gly Thr Val Gly

85

90

95

ctc gcc ccg gaa ccc atg cac ggc cgg gtc tcc gag gtg cgg cac acc 336

Leu Ala Pro Glu Pro Met His Gly Arg Val Ser Glu Val Arg His Thr

100

105

110

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ggc gag gac gtc ttc cgg ggc ctc ccc tcg ccg ttc acc gcc gtg cgc 384

Gly Glu Asp Val Phe Arg Gly Leu Pro Ser Pro Phe Thr Ala Val Arg

115

120

125

tac cac tcc ctg gcc gcc acc gac ctc ccc gac gag ctc gaa ccc ctc 432

Tyr His Ser Leu Ala Ala Thr Asp Leu Pro Asp Glu Leu Glu Pro Leu

130

135

140

gcc tgg agc gac gac ggg gtc gtc atg ggc ctg cgg cac cgc gag aag 480

Ala Trp Ser Asp Asp Gly Val Val Met Gly Leu Arg His Arg Glu Lys

145

150

155

160

ccg ctg tgg ggc gtc cag ttc cac ccg gag tcc atc ggc agc gac ttc 528

Pro Leu Trp Gly Val Gln Phe His Pro Glu Ser Ile Gly Ser Asp Phe

165

170

175

ggc cgg gag atc atg gcc aac ttc cgc gac ctc gcc ctc gcc cac cac 576

Gly Arg Glu Ile Met Ala Asn Phe Arg Asp Leu Ala Leu Ala His His

180

185

190

cgg gca cgg cgc cac ggg gcc gac tcc ccg tac gaa ctc cac gtg cgc 624

Arg Ala Arg Arg His Gly Ala Asp Ser Pro Tyr Glu Leu His Val Arg

195

200

205

cgc gtc gac gtg ctg ccg gac gcc gaa gag gta cgc cgc ggc tgc ctg 672

Arg Val Asp Val Leu Pro Asp Ala Glu Glu Val Arg Arg Gly Cys Leu

210

215

220

ccc ggc gag ggc acc acg ttc tgg ctg gac agc agc tcc gtc ctc gaa 720

Pro Gly Glu Gly Thr Thr Phe Trp Leu Asp Ser Ser Ser Val Leu Glu
 225 230 235 240

ggc gcc tcg cgc ttc tcc ttc ctc ggc gac gac cgc ggc ccg ctc gcc 768
 Gly Ala Ser Arg Phe Ser Phe Leu Gly Asp Asp Arg Gly Pro Leu Ala
 245 250 255

gag tac ctc acc tac cgc gtc gcc gac ggc gtc gtc tcc gtc cgc ggc 816
 Glu Tyr Leu Thr Tyr Arg Val Ala Asp Gly Val Val Ser Val Arg Gly
 260 265 270

tcc gac ggc acc acg acc cgg acg cgg cgc ccc ttc ttc aac tac ctg 864
 Ser Asp Gly Thr Thr Thr Arg Thr Arg Arg Pro Phe Phe Asn Tyr Leu
 275 280 285

gag gag cag ctc gaa cgc cga cgg gtc ccc gtc gcc ccc gaa ctg ccc 912
 Glu Glu Gln Leu Glu Arg Arg Arg Val Pro Val Ala Pro Glu Leu Pro
 290 295 300

ttc gag ttc aac ctc ggc tac gtc ggc tac ctc ggc tac gag ctg aag 960
 Phe Glu Phe Asn Leu Gly Tyr Val Gly Tyr Leu Gly Tyr Glu Leu Lys
 305 310 315 320

gcg gag acc acc ggc gac ccc gcg cac cgg tcc ccg cac ccc gac gcc 1008
 Ala Glu Thr Thr Gly Asp Pro Ala His Arg Ser Pro His Pro Asp Ala
 325 330 335

gcg ttc ctc ttc gcc gac cgc gcc atc gcc ctc gac cac cag gaa ggc 1056
 Ala Phe Leu Phe Ala Asp Arg Ala Ile Ala Leu Asp His Gln Glu Gly

340	345	350	
tgc tgc tac ctg ctg gcc ctc gac cgc cgg ggc cac gac gac ggc gcc			1104
Cys Cys Tyr Leu Leu Ala Leu Asp Arg Arg Gly His Asp Asp Gly Ala			
355	360	365	
cgc gcc tgg ctg cgg gag acg gcc gag acc ctc acc ggc ctg gcc gtc			1152
Arg Ala Trp Leu Arg Glu Thr Ala Glu Thr Leu Thr Gly Leu Ala Val			
370	375	380	
cgc gcc ccg gcc gag ccg acc ccc gcc atg gtc ttc ggg atc ccc gag			1200
Arg Ala Pro Ala Glu Pro Thr Pro Ala Met Val Phe Gly Ile Pro Glu			
385	390	395	400
gcg gcg gcc ggc ttc ggc ccc ctg gcc cgc gcg cgc cac gac aag gac			1248
Ala Ala Ala Gly Phe Gly Pro Leu Ala Arg Ala Arg His Asp Lys Asp			
405	410	415	
gcc tac ctc aag cgc atc gac gag tgc ctc aag gag atc cgc aac ggc			1296
Ala Tyr Leu Lys Arg Ile Asp Glu Cys Leu Lys Glu Ile Arg Asn Gly			
420	425	430	
gag tcg tac gag atc tgc ctg acc aac atg gtc acc gcg ccg acc gag			1344
Glu Ser Tyr Glu Ile Cys Leu Thr Asn Met Val Thr Ala Pro Thr Glu			
435	440	445	
gcg acg gcc ctg ccg ctc tac tcc gcg ctg cgc gcc atc agc ccc gtc			1392
Ala Thr Ala Leu Pro Leu Tyr Ser Ala Leu Arg Ala Ile Ser Pro Val			
450	455	460	

ccg tac ggc gcc ctg ctc gag ttc ccc gaa ctg tcg gtg ctg agc gcc 1440
 Pro Tyr Gly Ala Leu Leu Glu Phe Pro Glu Leu Ser Val Leu Ser Ala
 465 470 475 480

tcg ccc gag cgg ttc ctc acg atc ggc gcc gac ggc ggc gtc gag tcc 1488
 Ser Pro Glu Arg Phe Leu Thr Ile Gly Ala Asp Gly Gly Val Glu Ser
 485 490 495

aag ccc atc aag ggg acc cgc ccc cgg ggc ggc acc gcg gag gag gac 1536
 Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Gly Thr Ala Glu Glu Asp
 500 505 510

gag cgg ctc cgc gcc gac ctg gcc ggc cgg gag aag gac cgg gcc gag 1584
 Glu Arg Leu Arg Ala Asp Leu Ala Gly Arg Glu Lys Asp Arg Ala Glu
 515 520 525

aac ctg atg atc gtc gac ctg gtc cgc aac gac ctc aac agc gtc tgc 1632
 Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Asn Ser Val Cys
 530 535 540

gcg atc ggc tcc gtc cac gtg ccc cgg ctc ttc gag gtg gag acc tac 1680
 Ala Ile Gly Ser Val His Val Pro Arg Leu Phe Glu Val Glu Thr Tyr
 545 550 555 560

gcg ccc gtg cac cag ctg gtg tcg acc atc cgg gga cgg ctg cgg ccc 1728
 Ala Pro Val His Gln Leu Val Ser Thr Ile Arg Gly Arg Leu Arg Pro
 565 570 575

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ggc acc agc acc gcc gcc tgc gta cgc gcc gcc ttc ccc ggc ggc tcc 1776

Gly Thr Ser Thr Ala Ala Cys Val Arg Ala Ala Phe Pro Gly Gly Ser

580

585

590

atg acc ggc gcg ccc aag aag cgc acc atg gag atc atc gac cgc ctg 1824

Met Thr Gly Ala Pro Lys Lys Arg Thr Met Glu Ile Ile Asp Arg Leu

595

600

605

gag gaa ggc ccc cgg ggc gtc tac tcc ggg gcg ctc gga tgg ttc gcc 1872

Glu Glu Gly Pro Arg Gly Val Tyr Ser Gly Ala Leu Gly Trp Phe Ala

610

615

620

ctc agc ggc gcc gcc gac ctc agc atc gtc atc cgc acc atc gtg ctg 1920

Leu Ser Gly Ala Ala Asp Leu Ser Ile Val Ile Arg Thr Ile Val Leu

625

630

635

640

gcc gac ggc cag gcg gag ttc ggc gtc ggc ggg gcg atc gtg tcc ctc 1968

Ala Asp Gly Gln Ala Glu Phe Gly Val Gly Gly Ala Ile Val Ser Leu

645

650

655

tcc gac cag gag gag gag ttc acc gag acc gtg gta aag gcc cgc gcc 2016

Ser Asp Gln Glu Glu Glu Phe Thr Glu Thr Val Val Lys Ala Arg Ala

660

665

670

atg gtc acc gcc ctc gac ggc agc gcc gtg gcg ggc gcc cga tga 2061

Met Val Thr Ala Leu Asp Gly Ser Ala Val Ala Gly Ala Arg

675

680

685

<210> 2

<211> 686

<212> PRT

<213> *Streptomyces venezuelae*

<400> 2

Met Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Phe Thr His Asn Leu

1

5

10

15

Phe Gln Tyr Ile Gly Glu Ala Thr Gly Gln Pro Pro Val Val Val Pro

20

25

30

Asn Asp Ala Asp Trp Ser Arg Leu Pro Val Glu Asp Phe Asp Ala Ile

35

40

45

Val Val Ser Pro Gly Pro Gly Ser Pro Asp Arg Glu Arg Asp Phe Gly

50

55

60

Ile Ser Arg Arg Ala Ile Thr Asp Ser Gly Leu Pro Val Leu Gly Val

65

70

75

80

Cys Leu Gly His Gln Gly Ile Ala Gln Leu Phe Gly Gly Thr Val Gly

85

90

95

Leu Ala Pro Glu Pro Met His Gly Arg Val Ser Glu Val Arg His Thr

100

105

110

Gly Glu Asp Val Phe Arg Gly Leu Pro Ser Pro Phe Thr Ala Val Arg

115

120

125

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Tyr His Ser Leu Ala Ala Thr Asp Leu Pro Asp Glu Leu Glu Pro Leu
130 135 140

Ala Trp Ser Asp Asp Gly Val Val Met Gly Leu Arg His Arg Glu Lys
145 150 155 160

Pro Leu Trp Gly Val Gln Phe His Pro Glu Ser Ile Gly Ser Asp Phe
165 170 175

Gly Arg Glu Ile Met Ala Asn Phe Arg Asp Leu Ala Leu Ala His His
180 185 190

Arg Ala Arg Arg His Gly Ala Asp Ser Pro Tyr Glu Leu His Val Arg
195 200 205

Arg Val Asp Val Leu Pro Asp Ala Glu Glu Val Arg Arg Gly Cys Leu
210 215 220

Pro Gly Glu Gly Thr Thr Phe Trp Leu Asp Ser Ser Ser Val Leu Glu
225 230 235 240

Gly Ala Ser Arg Phe Ser Phe Leu Gly Asp Asp Arg Gly Pro Leu Ala
245 250 255

Glu Tyr Leu Thr Tyr Arg Val Ala Asp Gly Val Val Ser Val Arg Gly
260 265 270

Ser Asp Gly Thr Thr Thr Arg Thr Arg Arg Pro Phe Phe Asn Tyr Leu

10/28

275

280

285

Glu Glu Gln Leu Glu Arg Arg Arg Val Pro Val Ala Pro Glu Leu Pro

290

295

300

Phe Glu Phe Asn Leu Gly Tyr Val Gly Tyr Leu Gly Tyr Glu Leu Lys

305

310

315

320

Ala Glu Thr Thr Gly Asp Pro Ala His Arg Ser Pro His Pro Asp Ala

325

330

335

Ala Phe Leu Phe Ala Asp Arg Ala Ile Ala Leu Asp His Gln Glu Gly

340

345

350

Cys Cys Tyr Leu Leu Ala Leu Asp Arg Arg Gly His Asp Asp Gly Ala

355

360

365

Arg Ala Trp Leu Arg Glu Thr Ala Glu Thr Leu Thr Gly Leu Ala Val

370

375

380

Arg Ala Pro Ala Glu Pro Thr Pro Ala Met Val Phe Gly Ile Pro Glu

385

390

395

400

Ala Ala Ala Gly Phe Gly Pro Leu Ala Arg Ala Arg His Asp Lys Asp

405

410

415

Ala Tyr Leu Lys Arg Ile Asp Glu Cys Leu Lys Glu Ile Arg Asn Gly

420

425

430

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Glu Ser Tyr Glu Ile Cys Leu Thr Asn Met Val Thr Ala Pro Thr Glu
435 440 445

Ala Thr Ala Leu Pro Leu Tyr Ser Ala Leu Arg Ala Ile Ser Pro Val
450 455 460

Pro Tyr Gly Ala Leu Leu Glu Phe Pro Glu Leu Ser Val Leu Ser Ala
465 470 475 480

Ser Pro Glu Arg Phe Leu Thr Ile Gly Ala Asp Gly Gly Val Glu Ser
485 490 495

Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Gly Thr Ala Glu Glu Asp
500 505 510

Glu Arg Leu Arg Ala Asp Leu Ala Gly Arg Glu Lys Asp Arg Ala Glu
515 520 525

Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Asn Ser Val Cys
530 535 540

Ala Ile Gly Ser Val His Val Pro Arg Leu Phe Glu Val Glu Thr Tyr
545 550 555 560

Ala Pro Val His Gln Leu Val Ser Thr Ile Arg Gly Arg Leu Arg Pro
565 570 575

Gly Thr Ser Thr Ala Ala Cys Val Arg Ala Ala Phe Pro Gly Gly Ser
580 585 590

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Met Thr Gly Ala Pro Lys Lys Arg Thr Met Glu Ile Ile Asp Arg Leu
595 600 605

Glu Glu Gly Pro Arg Gly Val Tyr Ser Gly Ala Leu Gly Trp Phe Ala
610 615 620

Leu Ser Gly Ala Ala Asp Leu Ser Ile Val Ile Arg Thr Ile Val Leu
625 630 635 640

Ala Asp Gly Gln Ala Glu Phe Gly Val Gly Gly Ala Ile Val Ser Leu
645 650 655

Ser Asp Gln Glu Glu Glu Phe Thr Glu Thr Val Val Lys Ala Arg Ala
660 665 670

Met Val Thr Ala Leu Asp Gly Ser Ala Val Ala Gly Ala Arg
675 680 685

<210> 3

<211> 312

<212> DNA

<213> *Streptomyces venezuelae*

<220>

<221> CDS

<222> (1).. (309)

<400> 3

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15

ctc gac ggg acg ctc ctg gac acg gtg cgg cgc cgc atc gac ctc ggt 96

Leu Asp Gly Thr Leu Leu Asp Thr Val Arg Arg Arg Ile Asp Leu Gly

20

25

30

gtc cgc atc gcg cgg tac aag tcc cgg cac ggc gtc ccg atg atg cag 144

Val Arg Ile Ala Arg Tyr Lys Ser Arg His Gly Val Pro Met Met Gln

35

40

45

ccc ggc cgg gtc agc ctg gtc aag gac agg gcc gcc cgc tac gcc gcc 192

Pro Gly Arg Val Ser Leu Val Lys Asp Arg Ala Ala Arg Tyr Ala Ala

50

55

60

gac cac ggc ctc gac gaa tcg ttc ctg gtg aac ctc tac gac gtg atc 240

Asp His Gly Leu Asp Glu Ser Phe Leu Val Asn Leu Tyr Asp Val Ile

65

70

75

80

atc acg gag atg tgc cgc gtc gag gac ctg gtg atg agc cgg gag agc 288

Ile Thr Glu Met Cys Arg Val Glu Asp Leu Val Met Ser Arg Glu Ser

85

90

95

ctg acg gcc gag gac cgg cgg tga

312

Leu Thr Ala Glu Asp Arg Arg

100

<210> 4

<211> 103

<212> PRT

<213> *Streptomyces venezuelae*

<400> 4

Met Thr Glu Gln Asn Glu Leu Gln Arg Leu Arg Ala Glu Leu Asp Ala

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10

15

Leu Asp Gly Thr Leu Leu Asp Thr Val Arg Arg Arg Ile Asp Leu Gly

20

25

30

Val Arg Ile Ala Arg Tyr Lys Ser Arg His Gly Val Pro Met Met Gln

35

40

45

Pro Gly Arg Val Ser Leu Val Lys Asp Arg Ala Ala Arg Tyr Ala Ala

50

55

60

Asp His Gly Leu Asp Glu Ser Phe Leu Val Asn Leu Tyr Asp Val Ile

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Ile Thr Glu Met Cys Arg Val Glu Asp Leu Val Met Ser Arg Glu Ser

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Leu Thr Ala Glu Asp Arg Arg

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<210> 5

<211> 969

<212> DNA

<213> *Streptomyces venezuelae*

<220>

<221> CDS

<222> (1).. (966)

<400> 5

atg agc ggc ttc ccc cgc agc gtc gtc gtc ggc ggc agc ggg gcg gtg 48

Met Ser Gly Phe Pro Arg Ser Val Val Val Gly Gly Ser Gly Ala Val

1

5

10

15

ggc ggc atg ttc gcc ggg ctg ctg cgg gag gcg ggc agc cgc acg ctc 96

Gly Gly Met Phe Ala Gly Leu Leu Arg Glu Ala Gly Ser Arg Thr Leu

20

25

30

gtc gtc gac ctc gta ccg ccg ccg gga cgg ccg gac gcc tgc ctg gtg 144

Val Val Asp Leu Val Pro Pro Pro Gly Arg Pro Asp Ala Cys Leu Val

35

40

45

ggc gac gtc acc gcg ccg ggg ccc gaa ctc gcg gcc gcc ctc cgg gac 192

Gly Asp Val Thr Ala Pro Gly Pro Glu Leu Ala Ala Ala Leu Arg Asp

50

55

60

gcg gac ctc gtc ctg ctc gcc gta cac gag gac gtg gcc ctc aag gcc 240

Ala Asp Leu Val Leu Leu Ala Val His Glu Asp Val Ala Leu Lys Ala

65

70

75

80

gtg gcg ccc gig acc cgg ctc atg cgg ccg ggc gcg ctg ctc gcc gac 288

Val Ala Pro Val Thr Arg Leu Met Arg Pro Gly Ala Leu Leu Ala Asp

85

90

95

acc ctg tcc gtc cgg acg ggc atg gcc gcg gag ctc gcg gcc cac gcc 336

Thr Leu Ser Val Arg Thr Gly Met Ala Ala Glu Leu Ala Ala His Ala

100

105

110

ccc ggc gtc cag cac gtg ggc ctc aac ccg atg ttc gcc ccc gcc gcc 384

Pro Gly Val Gln His Val Gly Leu Asn Pro Met Phe Ala Pro Ala Ala

115

120

125

ggc atg acc ggc cga ccc gtg gcc gcc gtg gtc acc agg gac ggg ccg 432

Gly Met Thr Gly Arg Pro Val Ala Ala Val Val Thr Arg Asp Gly Pro

130

135

140

ggc gtc acg gcc ctg ctg cgg ctc gtc gag ggc ggc ggc ggc agg ccc 480

Gly Val Thr Ala Leu Leu Arg Leu Val Glu Gly Gly Gly Gly Arg Pro

145

150

155

160

gta cgg ctc acg gcg gag gag cac gac cgg acg acg gcg gcc acc cag 528

Val Arg Leu Thr Ala Glu Glu His Asp Arg Thr Thr Ala Ala Thr Gln

165

170

175

gcc ctg acg cac gcc gig ctc ctc tcc ttc ggg ctc gcc ctc gcc cgc 576

Ala Leu Thr His Ala Val Leu Leu Ser Phe Gly Leu Ala Leu Ala Arg

		17/28	
180	185		190
ctc ggc gtc gac gtc cgg gcc ctg gcg gcg acg gca ccg ccg ccc cac 624			
Leu Gly Val Asp Val Arg Ala Leu Ala Ala Thr Ala Pro Pro Pro His			
195	200		205
cag gtg ctg ctc gcc ctc ctg gcc cgt gtg ctc ggc ggc agc ccc gag 672			
Gln Val Leu Leu Ala Leu Leu Ala Arg Val Leu Gly Gly Ser Pro Glu			
210	215		220
gtg tac ggg gac atc cag cgg tcc aac ccc cgg gcg gcg tcc gcg cgc 720			
Val Tyr Gly Asp Ile Gln Arg Ser Asn Pro Arg Ala Ala Ser Ala Arg			
225	230	235	240
cgg gcg ctc gcc gag gcc ctg cgc tcc ttc gcc gcg ctg gtc ggc gac 768			
Arg Ala Leu Ala Glu Ala Leu Arg Ser Phe Ala Ala Leu Val Gly Asp			
	245	250	255
gac ccg gac cgt gcc gac gcc ccc ggg cgc gcc gac gcc ccc ggc cat 816			
Asp Pro Asp Arg Ala Asp Ala Pro Gly Arg Ala Asp Ala Pro Gly His			
260	265		270
ccc ggg gga tgc gac ggc gcc ggg aac ctc gac ggc gtc ttc ggg gaa 864			
Pro Gly Gly Cys Asp Gly Ala Gly Asn Leu Asp Gly Val Phe Gly Glu			
275	280		285
ctc cgc cgg ctc atg gga ccg gag ctc gcg gcg ggc cag gac cac tgc 912			
Leu Arg Arg Leu Met Gly Pro Glu Leu Ala Ala Gly Gln Asp His Cys			
290	295		300

cag gag ctg ttc cgc acc ctc cac cgc acc gac gac gaa ggc gag aag 960
 Gln Glu Leu Phe Arg Thr Leu His Arg Thr Asp Asp Glu Gly Glu Lys
 305 310 315 320

gac cga tga 969
 Asp Arg

<210> 6

<211> 322

<212> PRT

<213> Streptomyces venezuelae

<400> 6

Met Ser Gly Phe Pro Arg Ser Val Val Val Gly Gly Ser Gly Ala Val
 1 5 10 15

Gly Gly Met Phe Ala Gly Leu Leu Arg Glu Ala Gly Ser Arg Thr Leu
 20 25 30

Val Val Asp Leu Val Pro Pro Pro Gly Arg Pro Asp Ala Cys Leu Val
 35 40 45

Gly Asp Val Thr Ala Pro Gly Pro Glu Leu Ala Ala Ala Leu Arg Asp
 50 55 60

Ala Asp Leu Val Leu Leu Ala Val His Glu Asp Val Ala Leu Lys Ala
 65 70 75 80

Val Ala Pro Val Thr Arg Leu Met Arg Pro Gly Ala Leu Leu Ala Asp

85

90

95

Thr Leu Ser Val Arg Thr Gly Met Ala Ala Glu Leu Ala Ala His Ala

100

105

110

Pro Gly Val Gln His Val Gly Leu Asn Pro Met Phe Ala Pro Ala Ala

115

120

125

Gly Met Thr Gly Arg Pro Val Ala Ala Val Val Thr Arg Asp Gly Pro

130

135

140

Gly Val Thr Ala Leu Leu Arg Leu Val Glu Gly Gly Gly Gly Arg Pro

145

150

155

160

Val Arg Leu Thr Ala Glu Glu His Asp Arg Thr Thr Ala Ala Thr Gln

165

170

175

Ala Leu Thr His Ala Val Leu Leu Ser Phe Gly Leu Ala Leu Ala Arg

180

185

190

Leu Gly Val Asp Val Arg Ala Leu Ala Ala Thr Ala Pro Pro Pro His

195

200

205

Gln Val Leu Leu Ala Leu Leu Ala Arg Val Leu Gly Gly Ser Pro Glu

210

215

220

Val Tyr Gly Asp Ile Gln Arg Ser Asn Pro Arg Ala Ala Ser Ala Arg

20/28

225 230 235 240

Arg Ala Leu Ala Glu Ala Leu Arg Ser Phe Ala Ala Leu Val Gly Asp

245 250 255

Asp Pro Asp Arg Ala Asp Ala Pro Gly Arg Ala Asp Ala Pro Gly His

260 265 270

Pro Gly Gly Cys Asp Gly Ala Gly Asn Leu Asp Gly Val Phe Gly Glu

275 280 285

Leu Arg Arg Leu Met Gly Pro Glu Leu Ala Ala Gly Gln Asp His Cys

290 295 300

Gln Glu Leu Phe Arg Thr Leu His Arg Thr Asp Asp Glu Gly Glu Lys

305 310 315 320

Asp Arg

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for

the pabAB gene

<400> 7

gggggggatcc tatgcgcacg ctctgatcg ac

32

<210> 8

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the pabAB gene

<400> 8

gggggggatcc tcatcgggcg cccgccactg cg

32

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the papA gene

<400> 9

ggtgatcata tgcgcacgct tctgatcgac

30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the papA gene

<400> 10

ggtgatcatc atcgggcgcc cgccactgcg

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<210> 11

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the papB gene

<400> 11

gcggatccat atgaccgagc agaacgagct g

31

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the papB gene

<400> 12

gcggatcctc accgccggtc ctcggc

26

<210> 13

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the papC gene

<400> 13

gcggatccat atgagcggct tccccgca

29

<210> 14

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the papC gene

<400> 14

gcggatcctc atcggtccit ctcgccttc

29

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the Abp1 gene

<400> 15

ctcaaaccag gaactctttc t

21

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the Abp1 gene

<400> 16

rgacatgtgg aaaccacatt ttg

23

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the Abp1 gene

<400> 17

abncgggggaa ttcgtgggtg gtagatcat gccv

34

<210> 18

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the Abp1 gene

<400> 18

abnbamgggg gatccttgat gggttttggg w

31

<210> 19

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the Abp1 gene

<400> 19

abcbamgggg gatcctaaac tcccatctat agc

33

<210> 20

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for
the Abp1 gene

<400> 20

abcbagggtc tagacgactc attgcagtga gtag

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<210> 21

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
site-directed mutagenesis

<400> 21

gatcagaagc gtgcgcattg ttaggttgat tgaatgggttt tgggaattg

49

<210> 22

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
site-directed mutagenesis

<400> 22

ctcgttctgc tcggtcattg ttaggttgat tgaatgggttt tgggaattg

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<210> 23

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer for
site-directed mutagenesis

<400> 23

cgggggaagc cgctcattgt taggttgatt gatgggtttt gggaattg

48